

## RECEIVED

## SEQUENCE LISTING

JUN 2 6 2001

TEOM CENTER 1600.2900

<110> Willson, Tracy
 Nicola, Nicos A.
 Hilton, Douglas J.
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 Zhang, Jian G.

<120> NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME

<130> Davies Collison Cave

<140> 09/688,286

<141> 2000-10-13

<150> 09/051,843

<151> 1998-06-29

<160> 11

<170> PatentIn Ver. 2.0

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<222> (61)..(1338)

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4:220b

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atg gcg cgg Met Ala Arg 1			Glu Le					108
acc gcc acc Thr Ala Thr								156
cct glg acg Pro Val Thr 35			Val Gl					204
tgg acg tgg Trp Thr Trp 50								252
tat ttt agt Tyr Phe Ser 65		p Āsp Gln						300
act cat cgt Thr His Arg			Leu As					348
gtg ggc tct Val Gly Ser								396

										agc Ser						492
										aca Thr 155						540
										caa Gln						588
										aaa Lys						636
										at <b>a</b> Ile						684
										gtg Val						732
										ctt Leu 235						780
										aat Asn						828
										caa Gln						876
att Ile	tta Leu	gag Glu 275	gtt Val	gaa Glu	gag Glu	gac Asp	aaa Lys 280	tgc Cys	cag Gln	aat Asn	tcc Ser	gaa Glu 285	tct Ser	gat Asp	aga Arg	924
aac Asn	atg Met 290	gag Glu	ggt Gly	aca Thr	agt Ser	tgt Cys 295	ttc Phe	caa Gln	ctc Leu	cct Pro	ggt Gly 300	gtt Val	ctt Leu	gcc Ala	gac Asp	972
gct Ala	gtc Val	tac Tyr	aca Thr	gtc Val	aga Arg	gta Val	aga Arg	gtc Val	aaa Lys	aca Thr	aac Asn	aag Lys	tta Leu	tgc Cys	ttt Phe	1020

•

			acc atg tta ctc Thr Met Leu Leu		1116				
	Ala Val Ala		ctc ctt ttt tac Leu Leu Phe Tyr 365		1164				
			cct gat cct ggc Pro Asp Pro Gly 380	_	1212				
		Gln Asn Asp	gat acc ctg cac Asp Thr Leu His 395		260				
			gaa gaa acg gat Glu Glu Thr Asp 410	5 5-5	.308				
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1

Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg 

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<210> 3

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<212> DNA

<213> Human IL-13 receptor alpha-chain

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gcc ggc ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca 156 Ala Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro 20 25 30

cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204

Impoint imposition for the same strong Ala Ser Ser Amily Ser Lew Imp

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		_				~			_	_		ata Ile	~	/ -	_	300
												att Ile				348
												¢ct Pro				396
												gag Glu 125				444
												atg Met				492
												tat Tyr				540
												gaa Glu				588
												acc Thr				636
												gtc Val 205				684
												tta Leu				732
gtg Val 225	aaa Lys	cct Pro	gat Asp	cct Pro	cca Pro 230	cat His	att Ile	aaa Lys	aac Asn	ctc Leu 235	tcc Ser	ttc Phe	cac His	aat Asn	gat Asp 240	780

cta ttt tat gaa gta gaa gtc aat aac agc caa act gag aca cat aat Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn 260 265 270										
gtt ttc tac gtc caa gag gct aaa tgt gag aat cca gaa ttt/gag aga Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg 275 280 285										
aat gtg gag aat aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp 290 295 300										
act ttg aac aca gtc aga ata aga gtc aaa aca aat aag tta tgc tat Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr 305 310 315 320	•									
gag gat gac aaa ctc tgg agt aat tgg agc caa gaa atg agt ata ggt Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly 325 330 335										
aag aag cgc aat tcc aca ctc tac ata acc atg tta ctc att gtt cca Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro 340 345 350										
gtc atc gtc gca ggt gca atc ata gta ctc ctg ctt tac cta aaa agg Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Tyr Leu Lys Arg 355 360 365										
ctc aag att att ata ttc cct cca att cct gat cct ggc aag att ttt Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe 370 375 380										
aaa gaa atg ttt gga gac cag aat gat gat act ctg cac tgg aag aag Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys 385 390 395 400										
tac gac atc tat gag aag caa acc aag gag gaa acc gac tct gta gtg Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val 405 410 415										
ctg ata gaa aac ctg aag aaa gcc tct cag tgatggagat aatttatttt Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln 420 425	1358									
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<213> Human IL-13 receptor alpha-chain

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Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Cys 1 5 10 15

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Ala Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro  $20 \\ 25 \\ 30$ 

Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile 35 40 45

Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp 50 55 60

Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu 65 70 75 80

Thr Arg Arg Ser Ile Glu Val Pro Leu Asm Glu Arg Ile Cys Leu Gln
85 90 95

Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu 100 105 110

Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val 115 120 125

Thr Clu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser 130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr 145 150 155 160

Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe 165 170 175

Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys 180 185 190

Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn 195 200 205

Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg 210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp

Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn 260 Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Lew Pro Asp 295 300 Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr 310 315 320 Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly 325 330 335 Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro 345 350 Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Tyr Leu Lys Arg 360 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe 370 375 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys 390 400 Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val 405 410 Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln <210> 5 <211> 30 <212> PRT <213> signal sequence of murine IL-3

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Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser 20 25 30

\*\*\*: \*\* 1. terminal FlA (ep.) pe fall

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aactccacct tctacaccac ctgatctaga
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Trp Ser Xaa Trp Ser
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Ala Ser Ile Ser Ser Ser Asp Tyr Lys Asp Asp Glu Ser Arg Thr Glu 1 5 10 15

Val Gln Pro Pro Val Thr Xaa Leu Ser Val 20 25